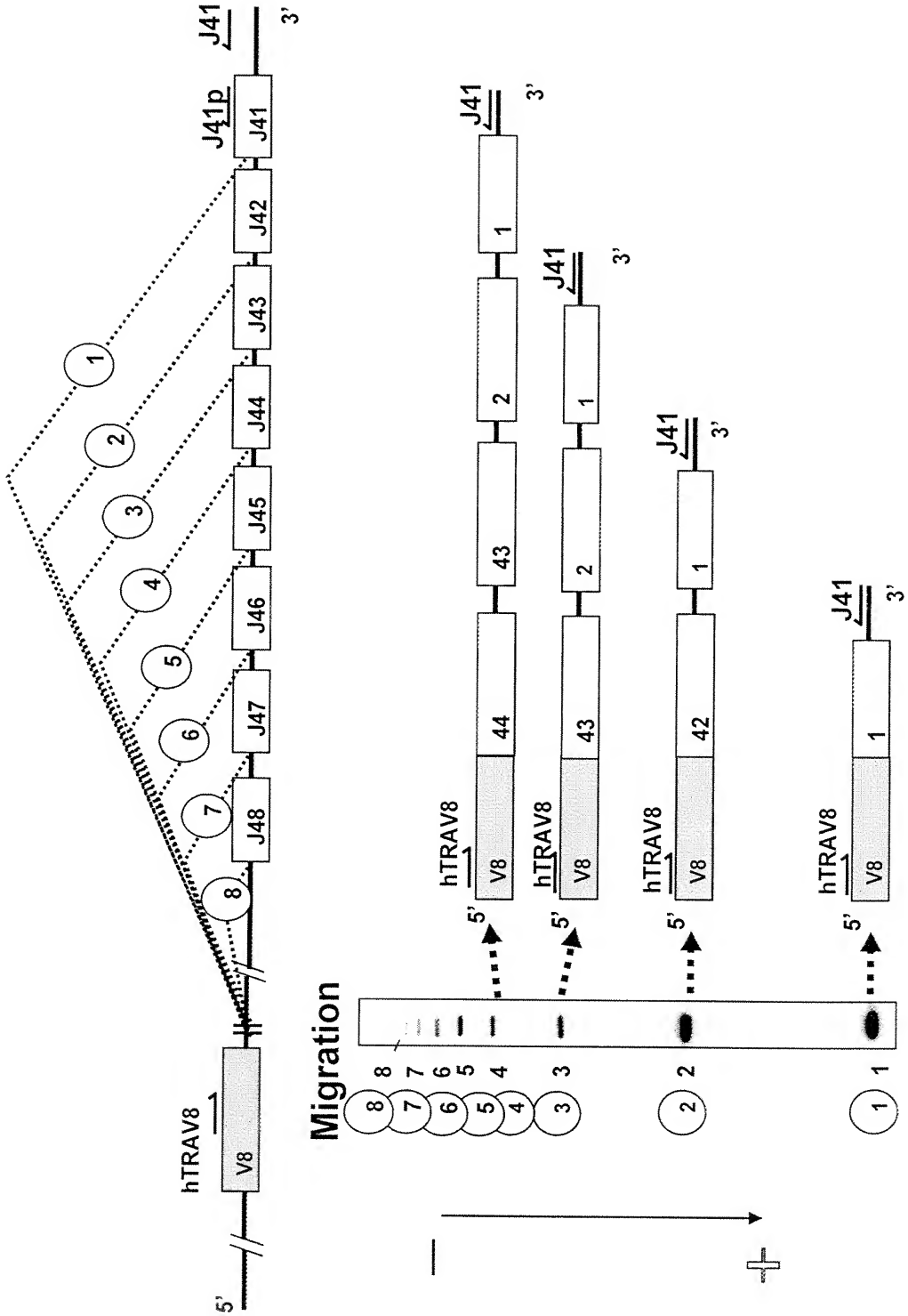


Figure 4



hv gene	Heptamer	SEQ ID NO	%	Spacer	SEQ ID NO	%	Nonamer	SEQ ID NO	%	RSS score	Dist/Cα (Kb)	Signal Qty	J tropism
hV1-1	CACAGTG	76	100	ACTATGAGGCGCTCTTTAACTGTG	77	56	CCAAATTC	78	56	<b>72</b>	925	1604	J10
hV1-2	CACGGTG	79	86	ACTATGAGGCGCTCTTTAGCTGCA	80	63	CCAAATTC	78	56	<b>69</b>	904	1637	J10
hV2	CACAGAG	81	86	GCAGGGAACCCCATGAACAGCTGA	82	56	ACAGAAACA	83	78	<b>75</b>	835	1940	J10
hV3	CACACTG	84	86	ATAGGGGCTGCGAGCGGAGGAGA	85	56	ACACAAACT	86	89	<b>80</b>	824	2406	J10
hV5	CACATTG	87	86	CTTCTCAGGCACTGTATCCCTGT	88	94	ACCCAAACC	89	100	<b>93</b>	798		J10
hV8-2	CACAGTG	76	100	CTTGAGACTGCAGGACAGCTGAA	90	50	CACAAGCCT	91	33	<b>63</b>	701	15830	All J
hV8-4	CACAGTG	76	100	CTTGAGACTGCAGGACAGCTGAA	90	50	CATAAACCT	92	33	<b>63</b>	653		area
hV8-6	CACAGTG	76	100	CCTGAGACTGCAGGACAGCTGAA	93	44	CACAACCT	94	44	<b>65</b>	569		
hV26-2	CACAGTG	76	100	GGACAGATGGGGCTGCAGCTGTG	95	56	CAATATCTC	96	33	<b>64</b>	345	5638	J48
hV35	CACAGTG	76	100	CTCCCAGAAACACCTGCTAGCCTGT	97	94	ACTCAAACCT	98	78	<b>90</b>	326	6520	J48
hV38-2	CACAGTG	76	100	AGACAAAGCAACAGGACAGGCTT	99	31	ACAGAAACC	100	89	<b>78</b>	267	11008	J48
hV40	CACITGT	101	86	TAAAAAGCACAGTGGAGGTATA	102	44	CAAAACCT	103	44	<b>60</b>	233	6930	J48
hV41	CACAGTG	76	100	CTCCCAGGCACTGGAGCCCT	104	94	ACCTAAACT	105	78	<b>90</b>	227	5630	J48
<b>Consensus</b>	CACAGTG	76		-T---CAG-CA-CTG-AACTGT G GC GG	106		ACACAAACC C	89		<b>%</b>			

FIGURE 5